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# The syndrome concept: history and statistical operationalizations

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**SYNOPSIS** A historical analysis of the syndrome concept shows that this term has been used in many different ways, ranging from clinical experience to records of coinciding symptoms. However, there seems to be broad agreement on the use of the word 'syndrome' in daily practice. If empirical–mathematical methods are applied in syndrome detection, however, a precise operationalization of the syndrome concept is needed. Traditional procedures have often used models more dictated by methodological considerations than derived from the field of application, i.e. psychiatric syndromatology. An alternative approach, Boolean factor analysis, is presented in this paper. This relatively new method is illustrated by means of the analysis of a small artificial sample with a known structure. As a point of reference, traditional methods (factor analysis, cluster analysis, and multidimensional scaling) are also briefly discussed. It is demonstrated that they all share a deficiency of information about inter-group structure. In contrast, Boolean factor analysis uses a syndromic definition which builds on the basic notion of concurrent symptoms. Moreover, this approach can easily be understood by clinicians.

## 1. HISTORY

Psychiatric nosology as reflected today by the International Classification of Diseases (ICD) (WHO, 1978) and other diagnostic systems should be based on a hypothetical entity of phenomenology (psychopathology), causation (aetiology), development (pathogenesis), course, outcome (possibly also treatment response), and morphological and/or physiological somatic grounds (neuropathology, pathophysiology). The realization of such an ideal nosology, however, is still out of reach so that the evaluation of syndromes becomes still more important. The search for such combinations of symptoms originates from Hippocrates, who attempted to find syndromes which would form typical clinical pictures of a disorder. 'Typos' (Greek) means 'Gestalt' or, more strictly, the picture, the imagination of a Gestalt.

Kahlbaum (1874) collected the most frequently coincident symptoms, thus constructing syndromes or types of disorders ('Krankheitsgestaltungen'). By so doing, he was able to define catatonia and hebephrenia (the

latter was well described by his pupil Hecker, 1871). Paranoia, the primary insanity of Snell (1865), is another branch of the same tree. This typology of mental illness became the basis of Kraepelin's nosology and, later on, of those of Eugen Bleuler, Kurt Schneider, and the modern classification of the World Health Organization (ICD).

Kleist, and later Leonhard, attempted to differentiate clinically observed syndromes by correlating them with localized brain dysfunctions and specific hereditary traits – thus producing a syndromatology rather than the intended nosology. Bonhoeffer (1910) correlated his concept of the acute exogenic reaction type with acute brain disorders of various types, but kept strictly to syndromatological research. This was exactly what Hoche (1912) postulated when he suggested that the search for symptom 'complexes' be improved. Later, Carl Schneider (1942) attempted to construct specific schizophrenic symptom combinations. All these attempts to generate syndromes were built on no more than clinical experience. The first attempt to establish a syndromatology based on empirical material was undertaken by Lorr *et al.* (1963).

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The criteria used for the construction of syndromes by various authors are quite different – for example, disordered psychological functions (consciousness, memory, orientation, mood, etc.), or correlations of clinical phenomena with supposed somatic disorders (psycho-organic, local brain, endocrine psychosyndrome, brain syndrome), or psychotraumatic life experience (psychogenic disorder). Another approach has been the construction of axis-syndromes (Berner, 1977), according to a previously defined nosological concept (organic *v.* endogenomorph, i.e. schizophrenic and cyclothymic).

In clinical experience the formation of syndromes is a Gestalt-psychological process which has its origin in the patient (as the symptom-producer), in the interviewer (the symptom-investigator), and in their mutual interactions. The observer brings to the process a set of personal, familial, cultural and professional norms and values, with internalized textbook-patterns of abnormal, even pathognomonic, behaviour and with standards of interaction with a patient. He may not only find the symptoms he is searching for, but also complete them to create syndromes according to his tendency to create a 'Gestalt' which was in his mind beforehand, i.e. symptoms may not merely be produced by the patient, but can represent the interaction between the patient and the environment induced by the professional interviewer. The same mechanisms apply even more to the construction of a syndrome which is essentially the creation of the psychiatrist, reflecting his interaction with the patient, the patient's expression of his needs, and the psychiatrist's intention to form clinical types and build up a psychopathological Gestalt.

Interview training, symptom checklists, operationalizations of definitions, and standardized diagnostic procedures can only in part correct the specialist's influence on the process of shaping a psychopathological type. We must bear this fact in mind when attempting to simulate the clinical process of syndrome construction by empirical methods. The combination of items representing a person's characteristic pattern of experience and behaviour is here evaluated by means of mathematical techniques for pattern recognition.

## 2. THE SYNDROME CONCEPT IN THE CONTEXT OF EMPIRICAL STUDIES

### Introduction

The preceding historical analysis shows that the term 'syndrome' has been used in many different ways. Yet though the definition of the term 'syndrome' rarely takes up more than a few lines in psychiatric textbooks, the word does not lead to much confusion in daily practice.

If electronic data processing is to be employed, however, a precise operational definition is required. The exact definition of a term whose use was previously vague often becomes necessary during the process of formalizing a scientific discipline. The strictly logical structure of computers renders this process obligatory. Before undertaking data analysis, a considerable amount of theoretical work must be carried out and fitted closely with the psychiatric terminology. As with Artificial Intelligence, the study of language calls for an understanding of computers and their capacities. To write computer programs to comprehend natural language we are obliged to study language itself in some depth. To construct a machine which is able to understand human speech one must first become a linguist.

One part of contemporary psychiatry deals with the analysis of large data sets with the aim of detecting natural 'syndromes'. The data base normally consists of lists of symptoms presented by large numbers of patients. The answers of each individual to a number of questions on his symptoms are registered in a standardized way. The so-called raw data table consists of the subjects' coded symptom scores on all the questions. The task of the data analyst is then to identify syndrome structures which may be hidden in the raw data table. We will call this procedure 'Automatic Syndrome Detection' (ASD).

### Automatic syndrome detection (ASD)

In ASD two interdependent problems have to be solved simultaneously:

- (1) the establishment of a well-defined syndrome concept which serves as a target structure to which the data are fitted;
  - (2) the identification of a data-analytical procedure which is appropriate to the task.
- Such a procedure belongs to the wider field of

pattern recognition which we cannot discuss further here.

As mentioned above, points (1) and (2) are closely related. Certain data-analytical procedures are flexible, allowing for a variety of syndrome concepts to be embedded in their algorithms. Others are tied conclusively to one model. Often, very little attention is paid to point (1). Multivariate statistical procedures are widely used, without an awareness of the kind of syndromic concept being employed. In most cases, consideration is given only to one formal property of syndromes, namely the fact that they are composed of *groups of symptoms*. Any statistical procedure imposing a group structure on the data is then usually applied, regardless of the respective grouping rule. Three procedures are most frequently used: factor analysis (FA), cluster analysis (CA), and multidimensional scaling (MDS).

In the present paper we shall discuss the role played by some of these methods in ASD without going into the mathematical details. In particular, we are concerned with some basic properties of the syndromic concepts they employ. We shall also present a relatively new procedure, called Boolean factor analysis, as an alternative approach.

### The detection of syndromes by computer

It has already been mentioned that syndromes formally comprise groups of symptoms. This is the most trivial property of any syndrome concept. What is the underlying principle which allows a certain number of symptoms to be called a 'syndrome'?

In medical terms it is, of course, the pathological process which causes the symptoms to appear. In many somatic diseases this process is well understood and a causal law can be established. In psychiatry, however, all that we can perceive is the *concurrence* of certain symptoms on a superficial level. In general, the underlying processes cannot be observed. Certain symptoms appear simultaneously and, when such regularities are repeatedly observed in many patients, we are inclined to assume a common origin and to call the relevant symptoms a 'syndrome'.

The statistical procedures to be discussed below do something quite different from simply

looking for groups of concurrent symptoms. Sometimes they use quite sophisticated models taken, for example, from Psychological Test Theory which expand the syndrome concept unnecessarily. In our view an expansion of the syndrome concept is frequently dictated only by the method used and does not correspond to any theoretical concepts in psychiatry. We find the concurrence of symptoms to constitute a satisfactory rule for the detection of syndromes and we present here a method especially appropriate for the identification of such structures.

### Boolean factor analysis: a simple syndrome concept and its corresponding algorithm

Boolean factor analysis (BOOLE-FA) makes direct use of raw data. No similarity matrices are involved. We first encountered this method in the 1981 version of the BMDP Statistical Software Package.<sup>1</sup> The method is based on research conducted by Engelmann *et al.* (1982) and the algorithm is described in the BMDP-81 manual. Based on this description, one of us (A.C.W.) wrote a FORTRAN-IV program to perform BOOLE-FA which at the same time has considerably extended the original program (see below).

Boolean algebra is a mathematical discipline dealing with set-theoretical operations, such as 'intersection' and 'union'. The second part of the name refers to a formal similarity in the way in which the raw data table can be decomposed into a 'loadings' and a 'scores' matrix. The operation used in this formula is of Boolean type. Apart from this formal analogy, which accounts for the similar names given to some resulting quantities, BOOLE-FA and FA have very little in common.

### An introductory example

Before going into technical details, we introduce BOOLE-FA by showing its effect on a simple artificial raw data table (Fig. 1).<sup>2</sup> This table is dichotomous, i.e. there are only two response categories, '1' for yes and '0' for no. Missing

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<sup>2</sup> All figures containing raw data tables are printed in condensed format and not in tabulated form in order to allow for immediate visual pattern recognition. In every case rows correspond to subjects and columns to items.

	1	2	3	4	5	6	7	8	9	10
1	1	1	1	1	0	0	1	1	0	1
2	1	1	1	0	1	1	0	1	1	1
3	1	1	1	0	1	1	0	1	1	0
4	1	1	1	1	0	0	1	1	0	1
5	1	1	0	1	0	0	1	1	0	1
6	1	0	1	0	1	1	0	1	1	0
7	1	1	1	0	0	0	0	1	0	0
8	0	0	0	0	0	0	0	0	0	0
9	1	0	1	0	0	1	0	1	1	0
10	1	1	1	0	0	0	0	1	0	0
11	1	1	1	0	1	1	0	1	1	0
12	0	0	0	0	0	0	1	0	0	0

FIG. 1. Artificial raw data table with a known structure. Rows = subjects; columns = items.

	1	2	3	4	5	6	7	8	9	10
1	1	1	1	1	0	0	1	1	0	1
2	1	1	1	0	1	1	0	1	1	0
3	1	1	1	0	1	1	0	1	1	0
4	1	1	1	1	0	0	1	1	0	1
5	1	1	1	1	0	0	1	1	0	1
6	1	1	1	0	1	1	0	1	1	0
7	1	1	1	0	0	0	0	1	0	0
8	0	0	0	0	0	0	0	0	0	0
9	1	1	1	0	1	1	0	1	1	0
10	1	1	1	0	0	0	0	1	0	0
11	1	1	1	0	1	1	0	1	1	0
12	0	0	0	0	0	0	0	0	0	0

FIG. 2. Reconstructed raw data table. Rows = subjects; columns = items.

Table 1. Loadings and scores matrices

Items/ subjects	Loadings	Scores
1	100	101
2	100	110
3	100	110
4	001	101
5	010	101
6	010	110
7	001	100
8	100	000
9	010	110
10	001	100
11	—	110
12	—	000

	1	2	3	8	5	6	9	4	7	10
2	1	1	1	1	1	1	1	0	0	0
3	1	1	1	1	1	1	1	0	0	0
6	1	1	1	1	1	1	1	0	0	0
9	1	1	1	1	1	1	1	0	0	0
11	1	1	1	1	1	1	1	0	0	0
1	1	1	1	1	0	0	0	1	1	1
4	1	1	1	1	0	0	0	1	1	1
5	1	1	1	1	0	0	0	1	1	1
7	1	1	1	1	0	0	0	0	0	0
10	1	1	1	1	0	0	0	0	0	0
8	0	0	0	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0	0	0

FIG. 3. Reconstructed raw data table rearranged. Rows = subjects; columns = items.

data are also allowed, but will not be discussed here.

First, we have to provide the program with a parameter denoting the number of 'factors'. In our example we used the value 3. (The role of the 'factors' is explained below.) The program then produces two lists, one called 'loadings' and one called 'scores' (Table 1). The rows of the table of loadings correspond to the items; the rows of the table of scores correspond to the subjects of the raw data. In both lists the columns correspond to the 'factors'.

What is the meaning of this decomposition? The easiest way to clarify the role of the 'factors' is to regard them as boxes. There are three boxes in this example. The loadings indicate how to distribute the items into the three boxes. If the loading of an item on a factor is '1', the item is put inside the box; otherwise, it is not. In this example, the distribution runs as follows:

Box 1: Items 1, 2, 3, 8.

Box 2: Items 5, 6, 9.

Box 3: Items 4, 7, 10.

The table of scores then determines the distribution of those boxes to the subjects following the same rule, which yields:

Box 1: to subjects 1, 2, 3, 4, 5, 6, 7, 9, 10, 11.

Box 2: to subjects 2, 3, 6, 9, 11.

Box 3: to subjects 1, 4, 5.

It should be noted that the subjects can be ascribed to more than one box. The same thing can happen with the loadings, but in the example given this is not the case.

With the help of these rules, we can construct a table of the same dimensions as the original raw data. We shall call this table the 'reconstructed raw data table' (Fig. 2).

The value of the procedure becomes evident immediately after the next step. The list of loadings and the list of scores allow us to rearrange both items and subjects according to their factor patterns. The sorting is done in such a way that elements with equal factor patterns are kept together. Fig. 3 shows the result of the rearrangement when applied to the reconstructed raw data table. The hidden structure of the raw



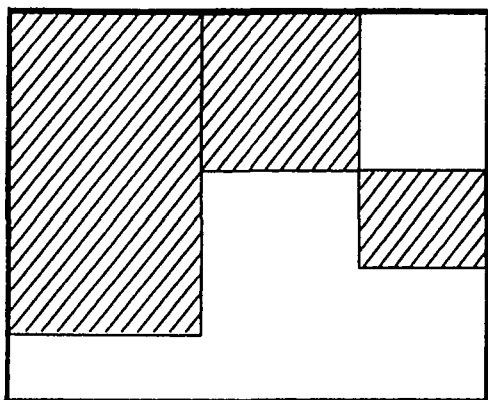


FIG. 4. Schematic representation of the block structure.

	1	2	3	8	5	6	9	4	7	10
2	1	1	1	1	1	1	1	0	0	1
3	1	1	1	1	1	1	1	0	0	0
6	1	0	1	1	1	1	1	0	0	0
9	1	0	1	1	0	1	1	0	0	0
11	1	1	1	1	1	1	1	0	0	0
1	1	1	1	1	0	0	0	1	1	1
4	1	1	1	1	0	0	0	1	1	1
5	1	1	0	1	0	0	0	1	1	1
7	1	1	1	1	0	0	0	0	0	0
10	1	1	1	1	0	0	0	0	0	0
8	0	0	0	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0	1	0

FIG. 5. Original raw data rearranged. Discrepancies to block structure model encircled. Rows = subjects; columns = items.

data is here made visible. The rearrangement results in a table composed of blocks of zeros and ones. Fig. 4 shows this structure schematically. The passage from a total of 10 items to a model with only 3 'boxes' necessarily results in a reduction of information and brings about a certain number of discrepancies compared with the raw data. Therefore, Fig. 3 has to be compared with a table of the original data rearranged in the same way (Fig. 5; discrepancies encircled). It can be seen that the raw data (Table 1) almost fit the model shown in Fig. 4.

There is, of course, no unique method of rearranging the data in order to reveal the block structure. The structure can be shown in different ways by rearranging entire blocks. The result depends on the rule that governs the sorting of items and subjects. We use the following algorithm. Each factor pattern, such as '110' or '010', can be regarded as a binary number ('110' = 6; '010' = 2), ranging from 0 to  $2^m - 1$ , with  $m$  denoting the number of factors.

We now simply rearrange subjects and items in descending order of the corresponding binary values.<sup>1</sup> This leads to a representation of the data where the number of positive responses roughly decreases from left to right and from top to bottom. Other ways of rearranging the data would be equivalent, as long as the members of a block are kept together correctly.

#### The algorithm

In a fashion formally analogous to factor analysis the raw data matrix  $X$  is decomposed as:

$$X = S * L + E,$$

where  $X = (x_{ij})$  is an  $n \times m$  matrix,  $S = (s_{ir})$  is the  $n \times p$  matrix of factor scores,  $L = (l_{jr})$  is the  $m \times p$  matrix of loadings,  $E = (e_{ij})$  is the  $m \times n$  matrix of residuals,  $n$  is the number of subjects,  $m$  is the number of items, and  $p$  is the number of factors. '\*' denotes the following operation:

$$(S * L)_{ij} = \begin{cases} 1 & \text{if for at least one factor } r \\ & (r = 1, \dots, p) s_{ir} = 1 \text{ and } l_{jr} = 1; \\ 0 & \text{otherwise.} \end{cases}$$

The algorithm tries to solve for a pair  $S, L$  which maximizes the number of zeros in  $E$ , i.e. it minimizes the number of discrepancies from the raw data. Starting with an arbitrary or read-in loadings matrix  $L$ , a double phase algorithm calculates, in turn, the optimal  $S$  for fixed  $L$ , and the optimal  $L$  for fixed  $S$ , using 'Boolean regression'. In order to explain Boolean regression we may consider the case of the calculation of a new row  $k$  of  $L$  for given  $X$  and fixed  $S$ .

(1) All  $l_{kr}$  ( $r = 1, \dots, p$ ) are set to zero.

(2) For every column  $r$  of  $(s_{ir})$ , an index  $M_r$  is computed:

$$M_r = \sum_i x_{ik} s_{ir} - \sum_i (1 - x_{ik}) s_{ir}.$$

(3) The column  $r^*$  containing the largest  $M_r$  is determined.

(4) If  $M_{r^*}$  is positive  $l_{kr^*}$  is set to one, and all entries of column  $k$  of  $X$  and of row  $i$  of  $S$  are set to zero if and only if  $s_{ir}$  contains a one.

Steps 2, 3 and 4 are repeated until the largest  $M_r$  is non-positive. The optimization of  $S$  takes place in the same way with the roles of  $L$  and  $S$  interchanged. After three cycles of double-phase iterations, the current number of factors  $p$  is either decreased or increased by one, following

<sup>1</sup> The sorting option is one of our extensions of the original program.

a 'three step forward, one step backward' rule until the desired  $p$  is reached. For a detailed description of this process, the reader is referred to the BMDP-81 manual.

Step 3 contains a typical problem of integer arithmetic. If the maximum of  $M_r (r = 1, \dots, p)$  is not unique, the selection of  $r^*$  is arbitrary. An optimal solution  $S, L$  may then be missed.

### *The syndrome model of BOOLE-FA*

What is the possible contribution of BOOLE-FA to ASD? It is our opinion that the blocks of BOOLE-FA form an appropriate operationalization of the syndrome concept as it is employed in psychiatric textbooks and used in daily practice. The concept of a block simultaneously fulfils the basic requirements of a syndrome concept and does not overload it. Syndromes are conceptualized as concurrent symptoms, and the subjects of the sample are either allocated a syndrome or they are not. There is no need to expand the meaning of the term 'syndrome' by introducing the notion of continuity and scales. A rearranged raw data table exhibiting a block structure is also comprehensible to a clinician with no knowledge of advanced statistics.

### **Traditional algorithms**

When BOOLE-FA is compared with the well-known 'ordinary' factor analysis (FA), the first point of interest is the implicit syndrome concept that enters into the use of FA for ASD purposes. It seems necessary to stress this because sometimes FA is applied by people who are unaware of the type of structure which is detectable by FA. Also, an illustrative example will be presented which constitutes the most trivial case of a syndrome structure and yet remains undiscovered by FA. Factor analysis was developed in the context of psychological testing. Typically, the subjects solve problems or answer questions about their personal likes and dislikes, about their attitudes or their values. It has been found that the subjects' answers are not randomly distributed. They seem to be guided by a small number of personality traits and, especially in intelligence testing, the manner in which the subjects solve the problems depends in some way on their 'intelligence', however this term is defined.

Traditionally, relations between quantitative variables (such as answers to questionnaire

items) have been measured by the so-called product-moment correlation coefficient. This is a number ranging from  $-1$  to  $+1$ , indicating the degree of dependency of two variables in a specific way. The correlation matrix serves as a basis for the construction of new 'hidden' variables – the factors – that 'explain' the structure of the matrix in a certain way. These factors are weighted sums of the original items and they are essentially *continuous* variables. This quality of factors can best be expressed by calling them 'scales'. *Factors are scales*. The model ascribes factor scores to the subjects, which indicate various degrees of how much a person possesses of that property. In the field of ASD, FA is used to construct syndromes and it is customary to identify the resulting factors as 'syndromes'. These syndromes then possess the continuous quality of scales, just like 'intelligence' or 'depression' in personality psychology. We do not regard this model as appropriate for the identification of syndromes, because a syndrome is typically non-continuous. If the subject is affected by the underlying illness – thus exhibiting certain syndromes – the symptoms are to appear; if he is not so affected, the symptoms should not be apparent. If we introduced the idea of continuity in the context of psychiatric syndromes we would have to give them names like 'schizophrenicity' or 'manicity' in order to clarify their scale property. Such a scale quality may sometimes intentionally be a part of a model when the syndrome construct under considerations is similar in nature to personality traits or to properties in general. In our opinion, however, the medical syndromes as conceptualized by medicine itself generally do not share that quality.

In fact, many advocates of FA employ this procedure without adopting the entire model that has been summarized above. They use it rather because of its incidental capacity to group the variables. The grouping is induced by the way the factors are constructed as weighted sums of the original variables. Through subsequent procedures, such as VARIMAX rotation, the weights are determined in such a way that distinct subgroups of the variables may possess high loadings on different factors. They are then referred to as identifying the property for which the factor stands. Obtaining groups of variables by means of the rotated loadings matrix can be

[illegible]

FIG. 6. Artificial raw data table with a simple structure.  
Rows = subjects; columns = items.

the only purpose of an FA. Nevertheless, the grouping mechanism follows the logic of continuous variables by providing a scale construction.

This process may now be compared with the syndrome model we presented in the introduction of BOOLE-FA. No matter whether that model is considered too simple or not, it should be understood that FA correctly detects the following simple case. Fig. 6 shows the yes/no answers of 30 subjects on 18 symptom items (yes = 1, no = 0). This table of artificial raw data simulates the most elementary case of three syndromes where there are three corresponding groups of subjects. Let them be called a 'simple syndrome structure of degree 3'.

FA now provides, surprisingly, exactly 2 factors, each accounting for 50% of the variance, meaning that the structure is totally explained by these two factors. A closer look at the so-called factor space (Fig. 7) explains this obvious contradiction. In the factor space the three syndromes form perfect clusters; in fact, all

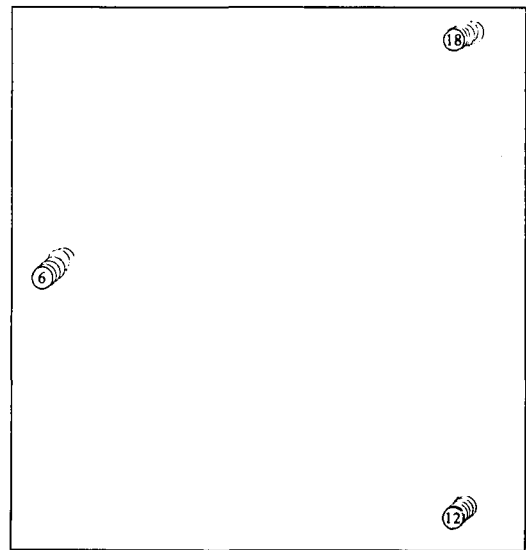


FIG. 7. Two-factor solution: factor space. Labels printed on top of each other:

1, 2, 3, 4, 5, 6;  
7, 8, 9, 10, 11, 12;  
13, 14, 15, 16, 17, 18.

the items of one group have the same position. It is the equation 'factor = syndrome' which leads to the wrong conclusions.

The correlation coefficient used in FA indeed rises with the degree of concurrence of the items. It shares this property with almost every other coefficient of similarity. Consequently, factors are likely to capture groups of frequently concurring symptoms. In many cases, therefore, ASD obtained by means of FA can lead to reasonable results, but the investigator can never be certain of its capacity to do so because FA takes items with high negative correlations (i.e. symptoms which do not concur at all) to belong to one and the same factor, although in a negative sense. They form the negative pole of the corresponding quality. This property of FA not only offers problems of interpretation, but it can also lead to strange results, as the example shows. In non-artificial data sets this property of FA interferes with a possibly more complex data structure and cannot be isolated and unmasked as easily as in our artificial example. Research based on the above equation can never guarantee that the factors found correspond to groups of concurring symptoms, even though in most instances this may be the case.



### ASD by means of cluster analysis (CA) and multidimensional scaling (MDS)

MDS and CA do not share the weakness mentioned above because they follow a different logical path. In contrast to FA, which employs a model based on the logic of correlational statistics, CA and MDS have weaker constraints and more flexibility. In a sense, they could be called 'neutral analysing devices' for similarity matrices. The performance of the algorithm depends on the choice of an appropriate similarity coefficient.

First, to clarify the idea of similarity/dissimilarity it is necessary to point out that we sometimes use the term 'similarity' in a more general sense. A matrix of similarity coefficients is a square table where the entry in row  $i$  and column  $j$  is a number denoting the degree of similarity (dependence, proximity, etc.) between elements  $i$  and  $j$ . A measure of similarity has to satisfy only two simple axioms: (1) Symmetry: the similarity between elements  $i$  and  $j$  has to be the same as that between elements  $j$  and  $i$ ; this is almost trivial. (2) There must be an upper bound to the possible range of values which is typically the value of the similarity of an element with itself. In the case of dissimilarity there must be a lower bound. A typical example of a table of dissimilarities is a distance table of the major towns of a country which can sometimes be found on road maps.

The matrix of correlation coefficients that FA accepts as input is an example of a matrix of similarities. The number in row  $i$  and column  $j$  denotes the degree of linear dependence of variables  $i$  and  $j$ . The product-moment correlation is probably the best known similarity coefficient.

Given a matrix of similarities, CA and MDS solve two slightly different but related tasks: (1) MDS tries to represent the objects as points in an Euclidean space so that the order of inter-point distances corresponds to the order of the similarity coefficients. Similar objects are clustered together, whereas dissimilar ones are represented by distant points. (2) CA tries to form groups directly without any representation as points in an Euclidean space. In this case it is not necessarily possible to visualize the obtained groups as clusters of points, a fact that suggests previous metrization through MDS.

In the context of ASD it is the symptoms that

form the elements – strictly speaking, the response vectors taken from each subject and the coefficient required has to be a measurement of concurrence. In the case of dichotomous items (see Fig. 6) Cohen's Kappa (Cohen, 1960) is an appropriate measure, since its logic derives from the percentage of concurrence.

In different applications specific similarity coefficients can be constructed which take into account specific properties of the respective discipline. Some work has been done to classify similarity coefficients and to establish something like a general theory of similarity (e.g. Cronbach & Gleser, 1958; Asendorff & Walbott, 1979), but without regard to these specific topics all similarity coefficients share the property of *continuity*.

In order to form a syndrome a certain number of symptoms should co-exist with no more than a few exceptions due to error. We believe that a continuous measure of concurrence does not exactly match the idea of a syndrome in psychiatry. Of course, if there is a syndrome structure in the data (as, for example, in Fig. 6) this will be detected because only a few discrete values of the similarity measure will appear. And if we computed the table of Kappa values for the data shown in Fig. 6, only two values would occur: 1.00 within syndromes, and -0.50 between.

It is only in the case of a continuous distribution of coefficients that interpretation becomes difficult. In this case, CA and MDS are unable to identify any stable groups, and different CA-algorithms yield different groupings. The data then do not fit a discontinuous model, and it is impossible to interpret them in terms of syndromes.

## DISCUSSION

Apart from the syndrome concept, there is another reason why, in our view, BOOLE-FA is superior to the other procedures. In contrast to them, BOOLE-FA omits the initial transformation of raw data into similarity measures. Although this transformation allows for sophisticated analyses, it also results in a specific loss of information. We are not referring here to the general loss of information due to inevitable data reduction, but to the particular loss of information concerning the relations *between* groups if

11111000001000000001	01111011110000000010
10111000000000000000	01111111110000000000
11110000000010000000	11111111110000000000
11111000000000010000	11101111010000000001
10110000000010000000	11111111110000000000
11111010000010000000	11001111010100000001
11110000000000000011	11011111111000000000
10111001101000000000	11110001110000000000
11010000000000001010	11111111110000000000
11111000000000001000	11111111110000000011
00000111010111000000	11111000000000100000
00000111111100000010	11101000100001001000
00000011110001000000	11111000000000000000
00000001110000000100	10110001000000100000
00101111111000000000	1111000001111100010
00000111110000000000	11111000001010100000
00000111110010000111	11111100001110100000
00011111110000000000	11011000001111100000
00000101110000000000	11111000010111101000
10000111110000000000	11111000001111100000
10000000001111100001	01111000001101111111
00100000001111100000	11111000001111111111
00000000001011100000	11110000001111110111
01000001001111100000	11111000001111111111
00000000000111111001	1111100000111101101
00100000001101100100	01000000001011111011
00000000001111101000	00000010001011111111
00000001001011100000	01110000001111111011
00000000001111100000	0000000100111011101
00001000001111100000	0000000000111111101
00001000000000111111	00000000001111100001
00000010000000001011	00000000001001110000
00100000100000111111	01010000001111100000
10000010000001011101	0000000010111100000
01010000000000011101	0000000000111100000
00000000000000001011	00001100001111100000
00000000000000001111	00000100001101101000
00000010100000010111	000000101111100100
00001000000001011111	000010000111100000
00100000000000011111	0000000000111100100

Figs. 9 and 10 show the corresponding MDS 2-space solutions. It should be kept in mind that, in the case of non-artificial data, the structure of the two raw data tables would be completely unknown, because both subjects and items would be arranged in an arbitrary order.

In both configurations the symptom groups are mapped into clusters of points. In both cases four groups are obtained, but only an expert data analyst can tell which configuration belongs to which table. It is the regularity in Fig. 9 which makes it likely to derive from Fig. 8(a). In other

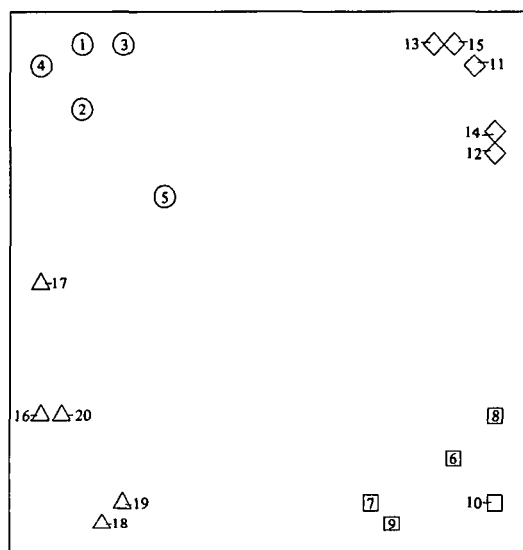


FIG. 9. MDS 2-space solution of the raw data in Fig. 8(a).

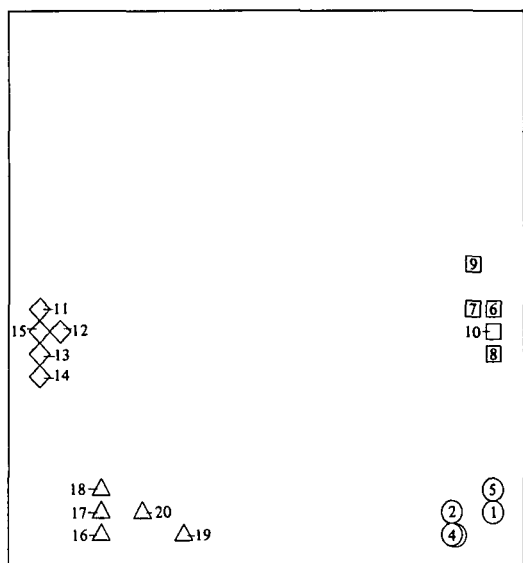


FIG. 10. MDS 2-space solution of the raw data in Fig. 8(b). Labels printed on top of each other: 3, 4.

cases where both structures are not simple, a distinction would be impossible. The equation 'group = syndrome', although correct, misses the important difference in inter-group relations. The two samples lead to completely different scientific insights about nosological structure. In the first example there are four distinct syndromes; in the second case there are two overlapping main syndromes, each accompanied by

an accessory syndrome. This difference becomes invisible at the moment of transformation of the raw data into similarity matrices and can only reappear if the block structure of the raw data is made visible through a suitable rearrangement of both subjects and items.

BOOLE-FA preserves the relevant information on the inter-group relations which is mostly lost with the methods using similarity matrices. This fact gives rise to a more complicated terminology concerning syndrome structures. It is not then necessary to be restricted to the mere statement of how many syndromes exist and what their members are. The relations between blocks could be described by terms like 'core syndrome' and 'accessory syndrome', depending on the complexity of the resulting structures. The blocks of the example could be called one 'general syndrome' with two possible complications or 'accessory syndromes'. In the case of more complicated structures new terms may be needed.

Another function of BOOLE-FA is to clarify multidimensional representations, should these be required. If, as is usually the case, there is no clear cluster structure, interpretation can become difficult. A Boolean block structure then does not fit the data and is loaded with a considerable amount of error. Nevertheless, the block structure can point out tendencies in the data which determine the regions of the spatial configuration.

Mention should also be made of the several weaknesses of the procedure. BOOLE-FA needs an initial table of loadings to initiate its circles of iterative optimization. In our program, this starting table is generated with random numbers and the result depends on the choice of starting point. Therefore it is necessary to try several starting positions in order to determine the best solution. With no underlying block structure (when the model is inappropriate), the solutions can vary considerably, but the weakness then lies also in the data themselves which resist attempts to have a block structure imposed on them.

Another weakness has already been touched upon. At one point of the algorithm the maximum of a set of integers has to be determined, and there are probably several elements with maximal values. The particular choice then depends on the arbitrary order of variables and subjects in the original raw data

table, leading to the uncomfortable situation that the solution depends on a meaningless order. However, since there is no reasonable choice between one maximal value and another no obvious solution to this problem presents itself.

Finally, we shall briefly examine the extensions of our BOOLE-FA program compared with the original:

(1) The main new feature is the sorting option, as explained in the text (see pp. 318–319).

(2) Closely related is a special output option which prints the rearranged tables with spaces between blocks. Subjects and variables are labelled with their original sequence numbers, which facilitates their identification.

(3) Optional label vectors are written in a way which can be read by other programs (e.g. MDS) in order to label the points of dimensional plots by their BOOLE-FA group codes, instead of their sequence numbers. This option makes it possible to relate traditional spatial representations to BOOLE-FA solutions.

(4) Our version allows for a maximum of 610 subjects and 160 variables. These limitations can easily be extended.

(5) For small problems the program can be called in interactive mode. Raw data tables of the order of  $50 \times 50$  cause no visible delays. Larger problems of about  $600 \times 100$  data values take

about 10 min computation time and are better treated in batch mode.

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